From:

Myers, Carla

Sent:

Wednesday, October 12, 2005 7:00 AM

To: Subject: STIC-Biotech/ChemLib sequence search 09/887941

Please do an oligomer search in commercial and interference files for fragments of SEQ ID NO: **11 and 12** - please limit the search results to nucleic acids of a length of 50 nucleotides or less.

Please provide a printout of the first 40 results.

The CRF has been entered; http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL\_ID=09887941

Thank you

Carla Myers AU 1634 Remsen Bldg / Rm 2E79 Mailbox: REM 2C70 571-272-0747

OCT 12 2005

Searcher:

Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

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 Vendors and cost where applicable
STN:
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Other (Specify):

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152 GCGGACAGAGCAGA 165 AUI07206 Sugano Homo sapiens c AUI07206 Sugano Homo sapiens c HRC10935, mRNA sequence. AUI07206 AUI07206 1 GI:13556727 EST. Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200
149-156 (1997) Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 50) Contact: Yutaka Suzuki Homo sapiens (human) GCGGACAGAGCAGA 33 Conservative /organism="Homo sapiens"
|mol type="maRA,"
|db xref=""taxon: 9606"
|clone="HRC10935"
|clone\_lib="Sugano Homo sapiens cDNA library" ocation/Qualifiers 7.1%; Score 14; DB; ; Pred. No. 2.7. 0; Mismatches bp mRNA linear EST 28-JAN-2004 cDNA library Homo sapiens cDNA clone 2.7e+04; hes 0; DB 1; Length 50 Indels Gene 200 (1-2), 0; Gaps 0

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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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KAT06101, mRNA sequence
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minaroku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A.
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A.
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science,
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese
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/mol Type="mRNA"
/db_xref="reaxon:9606"
/clone="HRC12745"
/clone_lib="Sugano Homo sapiens cDNA library"
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., (
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, I
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Institute of Medical Science, Uni
4-6-1, Shirokanedai, Minatoku, To
Email: ysuzuki@ims.u-tokyo.ac.jp
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                      Similarity
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                                                                     larity 100.0%;
Conservative 0;
                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG05636"
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/db xref="taxon:9606"
/clone="kRY06101"
/clone_lib="Sugano Homo sapiens cDNA library"
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                                                                                                                                               /clone="LNG05535"
/clone_lib="Sugano Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:13556732
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                                                                                      Score 14; DB 1; Li; Pred. No. 2.7e+04;
                                                                                                                                                                                                                                                                                                                                                                          Science, University of Tokyo
Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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2.7e+04;
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RESULT 5

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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Word size :
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                   15
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Match
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Gapop 60.0 , Gapext 60.0
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196
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                                                                                                                                                                                                                                                                                                                                         'Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US109_NEW_PUB.seq:*
'Cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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'Cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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'Cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06_PUBGOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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      US-10-098-263B-17480

US-10-719-900-56424

US-10-719-900-195425

US-10-719-900-489771

US-10-719-900-955757

US-10-719-956-180263

US-10-719-956-315460
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Sequence 17480, A Sequence 56424, A Sequence 195425, Sequence 489771, Sequence 955757, Sequence 180263, Sequence 315460,
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US-10-843-527-1700	US-10-843-527-68092	US-10-956-157-30819	US-10-956-157-1925	US-10-809-189-11250	US-10-809-189-11250	US-10-809-189-23342	US-10-719-900-88874	US-10-719-900-84384	US-10-719-900-83763	US-10-719-900-7652	US-10-719-900-76424	US-10-719-900-74731	US-10-719-900-69585	US-10-719-900-26767	US-10-719-900-20032	US-10-719-900-153	US-10-719-900-10913	US-10-719-900-10215	US-10-719-900-71312	US-10-098-263B-24	US-10-257-158A-43	US-10-257-158A-89	US-10-177-798-	US-10-235-463-	US-10-632-342	US-10-632-342-19	US-11-036-317-97	US-11-036-317-95736	US-11-036-317-93953	US-11-036-317-92736	US-11-036-317-89091	US-11-036-317-45273	US-11-036-317-36382	US-11-036-317-33964	US-11-036-317-30816	US-11-036-317-25796	US-11-036-317-20298
quence 170085,	ence 68092	quence 30819	quence 1925	quence 11250	quence 11250	Trence occurry,	mience 88874	Colfo compaña	guence 83763	duence 765	quence /4/31	78C69 aprianh	drence 79.97	quence 20032	Signature 19379	concerne 10	Squesice 10213	quence /131	Conesice 2131	equence 3346	Addence 933	rquerice 19,	rquence 39	quence 19		edience 10	aneance comercia	equence 95736	emience olosi	equence 92736	cdronce about	equence 45373	tocot pouch	equence 33964	ונה ה הוא	equence 25796	equence 20298

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 17480

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-17480 US-10-098-263B-17480 Sequence 17480, Application US/10098263B Publication No. US20030104410A1 GENERAL INFORMATION:
APPLICANT: Mittman, Michael TITLE OF INVENTION: Human Microarray FILE REFERENCE: 3118.1 Query Match Local 92 CAGGAACCTCAGAGA 106 w Similarity 100.0%; F 15; Conservative 0; 7.7%; Score 15; Pred. No. Mismatches DB 15; I Length 25; Indels 0, Gaps

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RESULT 3
US-10-719-900-195425/c
y Sequence 195425, Application US/10719900
publication No. US20050026164A1
US20050026164A1
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US-10-719-900-489771/c
US-10-719-900-489771, Application US/10719900
; Publication No. US20050026164A1
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; APPLICANT: Xue Mei Zhou
; APPLICANT: Xue Mei Zhou
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PRIOR FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 56424

LENGTH: 25

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APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
PRIOR FILING DATE: 2002 11 20
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Best Local :
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                     TITLE OF INVENTION: Methods of Genetic Analysis of Mouse FILE REFERENCE: 3528.1 CURRENT APPLICATION NUMBER: US/10/719,900 CURRENT FILING DATE: 2003-11-20 PRIOR APPLICATION NUMBER: 60/427,808 PRIOR FILING DATE: 2002 11 20 NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 489771
LENGTH: 25
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; TYPE: DNA; ORGANISM: Mus musculus US-10-719-900-489771
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US-10-719-900-955757
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                                                                                                                                                                                      ORGANISM: Rattus norvegicus US-10-719-956-180263
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RESULT 7
US-10-719-956-315460
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Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 955757
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                                                                                                                                                                                                                                SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 180263
LENGTH: 25
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR EILING DATE: 2002 11 20
                                                                                                                           Matches
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Methods of Genetic Analysis of Rat FILE REFERENCE: 3527.1 CURRENT APPLICATION NUMBER: US/10/719,956 CURRENT FILING DATE: 2003-11-20 PRIOR APPLICATION NUMBER: 60/427,836 PRIOR FILING DATE: 2002 11 20 PRIOR FILING DATE: 2002 11 20 PRIOR FILING DATE: 2002 11 20
                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 699466
                                                                                                                                                                                                                       TYPE: DNA
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[00.0%; Pred. No.
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100.0%; Pred. No. 1.
ive 0; Mismatches
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Maximum DB
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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        GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-09-366-108A-2615

US-09-866-108A-2616

US-09-866-108A-2619

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US-09-866-108A-2619

US-09-866-108A-2619

US-09-866-108A-2619

US-09-866-108A-2619

US-09-167-109-87

US-09-167-109-87

US-09-866-28-44

US-09-866-28-44

US-09-868-28-7

US-09-868-28-7

US-09-868-28-7

US-09-868-28-7

US-09-868-28-7

US-09-868-28-7

US-09-387-37

US-09-243-335-26

US-09-387-341-223

US-09-387-381-223

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Sequence 5, Appli
Sequence 2615, Ap
Sequence 2616, Ap
Sequence 2617, Ap
Sequence 2619, Ap
Sequence 2619, Ap
Sequence 86, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 70, Appl
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17, Appl
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17, Appl
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23342, A
112506,
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US-09-000-630C-17/c
US-09-000-630C-17/c
; Sequence 17, Application US/09000630C
; Patent No. 6018029
; GENERAL INFORMATION:
; APPLICANT: Fuller, Gerald M
APPLICANT: Fuentes, Nelson L.
; TITLE OF INVENTION: DNA Encoding Ca
; TITLE OF INVENTION: Antagonist
; NUMBER OF SEQUENCES: 27
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SEQ ID NO 19
LENGTH: 19
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Best Local S
CORRESPONDENCE ADDRESS:
ADDRESSEE: Douglas C Murdock/ Bradley,
STREET: 2001 Park Place, Suite 1400
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Canine

Interleukin-1

Receptor

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Gaps

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	67675,	59088,	59077,	46116,	12058,	8224,	5556,	5555,	5554,	5553,	5552,	5551,	5550,	5549,	5548,	5547,	5546,	5545,
5544, 5547, 5548, 5549, 5550, 5551, 5552, 5553, 5554, 5556, 8224, 112058, 1120	٠.	` ⊳				Ą	Ą	Ą	Αp	Ą	Ä	A	A	₽	Ą	A	₽	A

ALIGNMENTS

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FILE REFERENCE: 06275-165002

CURRENT APPLICATION NUMBER: US/09/422,936

CURRENT FILING DATE: 1999-10-22

PRIOR APPLICATION NUMBER: US 09/242,608

PRIOR FILING DATE: 1999-02-19

PRIOR PLIOR ON NUMBER: PCT/SE98/01947

PRIOR FILING DATE: 1998-10-27

PRIOR PLIOR DATE: 1998-10-27

PRIOR PRIOR DATE: 1997-10-27

PRIOR PLIOR DATE: 1997-10-27

PRIOR FILING DATE: 1997-10-27

PRIOR PRIOR PRIOR DATE: 1998-03-16

PRIOR PRIOR FILING DATE: 1998-03-16

PRIOR PRIOR PRIOR DATE: 1998-07-17

NUMBER OF SEQ ID NOS: 85

PRIOR FILING DATE: 1998-07-17

NUMBER OF SEQ ID NOS: 85
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Patent No. 646521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ekstrand, Jonas
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
FILE REFERENCE: 06275-165002
                                                                                                                                                                 TYPE: DNA ORGANISM: Rattus
118 AGGCCCGGGGAGAG 131
                                               l Similarity
14; Conserv
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                                                                    Score 14; DB 3; L
Pred. No. 1.5e+03;
                                                  Mismatches
                                                                                          Length 19;
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,

35203-2736

COUNTRY:

CITY: Birmingham

Alabama USA

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Best Local Similarity
Marches 14; Conserve
                                                                                                       ; MOLECULE TYPE: US-08-862-730C-17
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APPLICANT: Fuentes, N
TITLE OF INVENTION: D
TITLE OF INVENTION: A
NUMBER OF SEQUENCES:
                                Query Match
Best Local Similarity 100.0%; F
Matches 14; Conservative 0;
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                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Diskette, 3.50 inch, COMPUTER: IBM compatible OPERATING SYSTEM: Microsoft Windows SOFTWARE: Wordberfect 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/000,630C FILING DATE.
                                                                                                                                                                                                                                      COMPUTER: IBM compatible
OPERATING SYSTEM: Microsof
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400
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LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                 LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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109 GAGGCTGACAGGCC 122
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DNA Encoding Canine Interleukin-1 Receptor
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27
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                                           7.1%; Score 14; DB 3; 00.0%; Pred. No. 1.5e+C. Ve 0; Mismatches
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Pred. No.
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RESULT 6
US-09-396-196G-112507/c
US-09-206-112507, Application US/09396196G
; Patent No. 6821724
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                                                                                                                                                                                                                                                 ; TYPE: DNA ; ORGANISM: mus musculus US-09-396-196G-112506
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 112506
LENGTH: 25
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PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23342
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Best Local (
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Patent No. 6821724
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
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TITLE OF INVENTION: Methods of Genetic Analysis
FILE REPERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
CURRENT FILING DATE: 1999-09-15
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David Lockhart
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llarity 100.0%; Pred. No. 1.5e+03;
Conservative 0; Mismatches 0;
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GENERAL INFORMATION: APPLICANT: Michael Mittmann

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Aag10273 Probe B(I
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Aba01161 Human zin
Aba01161 Human zin
Adm34012 Human SCN
Aax58008 PCR prime
Abi97219 Capture o
Adj31930 Human orp
Aah62255 SLC1A6 po
Aat94895 Human GAB
Aal44783 Human GAB
Abi91008 Capture o
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Abi91009 Capture o
Aci24415 Human RGS
Aag29387 Neutral s
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RESULT 1
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XX EST;
KW Gene
KW CTOS
XX HOMC
XX US2C
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PD 05-C
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genetic variation;
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                                                                                                                                                                                                                                                                                                    cross-species comparison.
                                                                                                                                                                                 (AFFY-)
                                                                                                                                                                                                                    15-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  13-OCT-2003
                                                                                                                                                                                                                                                             US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                          Human microarray DNA oligonucleotide SEQ ID NO 17480.
                                                                                                                                                                                                                                                                                                                                                                                     ACI17489;
                                                                                                                                                                                                                                                                                                                                                                                                        ACI17489 standard; DNA;
                                                                                                                                                                               AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                           expressed sequence tag; microarray; gene expression;
on; biallelic marker; polymorphism; human;
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis

Claim 1;

SEQ ID NO 17480;

9pp; English.

New array of nucleic acid probes, useful for Southern, Northern or dot-blot hybridization sequence or specific mutations of any gene.

in situ hybridization, in to identify or detect the

WPI; 2003-567953/53.

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RESULT 2
ABA01159
ID ABA0
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                                         The present invention relates to human zinc finger protein 72 (see AAM52332). The zinc finger protein and its coding sequence are useful the diagnosis and treatment of cancer, haemopathy, HIV infection, immunological diseases, various inflammations, nervous system diseases and developmental disorders. The present sequence is a PCR primary was used in an example from the present.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                    diseases and various inflammations.
                                                                                                                                                                                                                                                                                                                                                                          New human zinc finger protein 72 for diagnosing and treating malignant
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Pred. No.
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            24-JAN-2002
                                 ABA01162;
                                                                                                                                                                                                Sequence 38
                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 26pp; English
                                                                                                                                                                                                                                                                                                                                           encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoarthritis; screening
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03-APR-1991
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                                                     ABA01162
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                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1989;
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                                                      standard;
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                                                      DNA; 41
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1.9e+03;
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196
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Copyright (c) 1993 - 2005 Compugen Ltd.
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CQ617877
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      CQ617875 Sequence
CQ617876 Sequence
CQ617877 Sequence
CQ617878 Sequence
CQ617879 Sequence
AR458938 Sequence
AR458939 Sequence
AR458941 Sequence
                                                                                      AR236573 Sequence
AX2971.77 Sequence
E13893 PCR primer
AX292244 Sequence
AX318212 Sequence
AX318212 Sequence
AX318214 Sequence
AX318214 Sequence
AX815626 Sequence
I88811 Sequence 5
M64562 Mouse JH-Cd
                                                                                                                                                                                    Description
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AX297177
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
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                                                                                                                                                   118 AGGCCCGGGGAGAG 131
                                                                                                                                                                                                                                                                               Unclassified.
1 (bases 1 to
Ekstrand, J.
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AR236573
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REFERENCE
AUTHORS
TITLE
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Sequence 8939 from Patent WO0179548.
AX297177
AX297177.1 GI:17058868
Barany,F., Zirvi,M., Gerry,N.P., Favis,R. Method of designing addressable array for
                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequences
Patent: US 6465213-A 19 15-OCT-2002;
Location/Qualifiers
                                        other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                   /organism="unknown"
/mol_type="genomic |
                                                                                                                                                                                                                                                      ; Score 14; DB
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0; Mismatches
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     and Kliman, R. detection of
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NEW G-PROTEIN CONJUGATED TYPE RECEPTOR PRINTED CONTROL TO SEP-1997;

PATENT: JP 1997238686-A 2 16-SEP-1997;

TAKEDA CHEM IND LTD

OS None

OC Artificial sequences.

PN JP 1997238686-A/2

PN JP 1997238686-A/2

PD 16-SEP-1997

PF 07-MAR-1996 JP 1996050678

PI HINUMA KUNIJI, FUJII AKIRA

PC C12N15/09,A61K48/00,C07H21/04,C12N1/
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                                                                                                  83 GATGAGTCCCAGGA 96
                                                                                                                             14;
                                                                                                                                                                                                                                                        PC G01N33/566//A61K39/395,(C12N1/21,C12R1:19),(C12P21/02,C12R1:19),(C12P21/08,PC C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH Key Location/Qualifiers
FH Source 1. 24
FT source /organism='Artificial sequences'.
          AX292544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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HINUMA KUNIJI, FUJII AKIRA
C12N15/09,A61K48/00,C07H21/04,C12N1/21,C12P21/02,C12P21/08,
                                                                                                                             Conservative
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wO 0179548-A 8939 25-OCT-2001;
RESEARCH FOUNDATION, INC. (US)
Location/Qualifiers
                                                                                                                                                                                        /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                           /organism='Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:3252660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="synthetic construct"
/mol type="unassigned DNA"
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100.0%;
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G protein-coupling receptor gene
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Sequence 13 :
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Use of the gaba b? receptor in assays to identify gamma hydroxybutyrate agonists, antagonists, and allosteric modulators
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                                                                                                                                                                                                                                                                                                                                                                                        Patent: WO 0190163-A 13 29-NOV-2001;
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                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
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                                                                                                                                                                                                                                                                          /note="PCR primer"
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/note="Hypothetical Probe
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GI:39646311
                              25 bp
from Patent W003066904.
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Post-processing:
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BH755587
AA732952
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CF310621
AZ513870
CL523870
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CG722869 1119073G0
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AJ732952 AJ732952
CL658678 PRI 0132a
CG7310621 ABF-0-05-F
AZ513870 11W0360K08
CL529376 HIV40G02.
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AU107543 AU107543
BX288916 Arabidops
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AZ5826891 MO375013
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AU25525 YW45609.81
AZ38692 ZM0115N15
AZ38692 ZM0115N15
AZ4868692 ZM0115N15
AZ486692 ZM0115N15
AZ486692 ZM0115N15
              BX656232
CF307411
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Class:
                                                                                                                                                                                                                                     Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST5874-NL.Se
                                                                                                                                                                                                                                                                                                                Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, Universitry of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1. (bases 1 to 40)
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PST5874-NL.Seg MICB1 Mus genomic survey sequence.
CL437571
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Contact: Hicks GG
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 Conservative 0;
                                                                                                                                                                                                                  Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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7.3%; Score 16; DB 9; Le 100.0%; Pred. No. 2.5e+03; lve 0; Mismatches 0;
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                           Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
                                                                      Maize genomic sequences
Unpublished (2001)
Contact: Walbot V
                                                                                                                                    Zea mays

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.
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AB094450 AB094450 GI:30307355
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Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                      Walbot, V.
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Small RNAs detected in the rice phloem sap
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Kannondail-25-2, Tsukuba, I
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Location/Qualifiers
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/clone_Tib="lambda TriplEx2 rice phloem sap cDNA"
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AUTHORS
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BH755587
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                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH755587 29 bp DNA linear GSS 01-MAR-2002 SALK 051892.52.10.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_051892.52.10.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                       Salk Institute Genomic Analysis Laboratory The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92 Tel: 858 453 4100 x1752 Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reverse complemented post-ligation sequence from source sequence. plate: 1119073 row: G column: 09 Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                     Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P. Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                        At2g38080.
                                                                                                                                               This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH755587.1
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//Clone_lib="1119 - RescueMu Grid AA"
//note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                      TDNA tagged
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
                                                                          Location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="nixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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/lab_host="DH10B"
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                        Score
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/ Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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      6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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  US-10-719-900-365536

US-10-719-900-616433

US-10-719-900-654770

US-10-719-900-717050

US-10-719-900-958924

US-11-036-317-20600

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Sequence 365536,
Sequence 616433,
Sequence 654770,
Sequence 717050,
Sequence 958924,
Sequence 23869, A
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## ALIGNMENTS

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RESULT 2
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Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
                                                                                                                                                                                                     US-10-719-900-365536
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US-10-719-900-365536
                                                                                                                             Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 365536
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
                                                                          155 CGTGCGACATTTCCCGAATTCTGCA 179
                                                      ш
                                                                                                                                              Similarity
                                                                                                                           11.4%; Score 25; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                      25
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0.011;
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                                                                                                                                 0,
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В Ş

US-10-719-900-616433

GENERAL INFORMATION:

Sequence 616433, Application US/10719900 Publication No. US20050026164A1

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Sequence 717050, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR PILING DATE: 2002 11 20

NUMBER OF SEG ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEPURGER: 0717050
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US-10-719-900-717050
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US-10-719-900-654770
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-616433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 98.9914
SOFTWARE: Microarray Probe Sequence Listing Generator SEQ ID NO 654770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 654770, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 616433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.4%; Score 25; Best Local Similarity 100.0%; Pred. No. Matches 25; Conservative 0; Mismatc
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
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11.4%; Score 25; DB
Local Similarity 100.0%; Pred. No. 0.0
hes 25; Conservative 0; Mismatches
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RESULT 7

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Sequence 958924, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER OF 520 ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 958924
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                                                                                                                                                           US-11-036-317-20600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mus musculus US-10-719-900-958924
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US-10-719-900-958924
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                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 20600
LENGTH: 25
TYPE: DNA
CORRANGEM: Microarray Probe Sequence Listing Generator V 1.1
                                                                                              Best
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                                                                                                                   Query Match
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Best Local
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les 25; Conserv
                                   150 CCGGCCGTGCGACATTTCCCGAATT 174
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25; Conservative 0;
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100.0%; Preu....
                                                                         11.4%; Score 25; DB 24;
100.0%; Pred. No. 0.011;
tive 0; Mismatches 0
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Pred. No.
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Pred. No. 0.011;
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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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Perfect score:
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      on:
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      nucleic search, using sw model
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Match
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Gapop 60.0 , Gapext 60.0
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220
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    Issued_Patents_NA:*
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                             Length
      GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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 US-08-857-946-149
US-08-970-740-149
US-08-970-740-150
US-08-970-740-150
US-08-970-740-150
US-08-413-813-41
US-08-447-346-41
US-08-438-759-30
US-08-438-759-30
US-08-438-759-30
US-08-117-361C-17
PCT-US94-05591-5
PCT-US94-05684-30
US-09-357-073-12
US-09-357-073-13
US-09-357-073-14
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US-09-357-073-15
US-09-357-073-19
US-09-357-073-19
US-09-396-196G-25595
US-09-396-196G-25595
US-09-396-196G-66126
US-09-396-196G-65126
US-09-396-196G-55137
US-09-253-396A-599
US-08-342-411A-32
PCT-US94-12883-32
US-08-036-5558-90
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                                       Sequence 149, App
Sequence 150, App
Sequence 150, App
Sequence 150, App
Sequence 41, Appl
Sequence 39, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 17, Appl
Sequence 18, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 613, Appl
Sequence 613, Appl
Sequence 66136, A
Sequence 66126, A
Sequence 66127, Appl
Sequence 66137, Appl
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Sequence
Sequence
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Sequence
               32,
32,
32,
                                                                        ; NAME/KEY: US-08-857-946-149
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            Query Match 9.1%; Score 20;
Best Local Similarity 100.0%; Pred. No.
Matches 20; Conservative 0; Mismatc
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CITY: BC
STATE: M
COUNTRY:
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US-08-734-664A-93	US-08-734-664A-90	US-08-735-021-93	US-08-735-021-90	US-08-470-335-93	US-08-470-335-90	US-08-671-978A-16	US-08-469-660-93	US-08-469-660-90	US-08-734-591A-93	US-08-734-591A-90	US-08-469-526A-93	US-08-469-526A-90	US-08-249-322A-93	US-08-249-322A-90	US-08-469-569-93	9	US-08-036-555B-93
Sequence 93, Appl	•	Sequence 93, Appl	90,	93,	e 90,	e 16,	e 93,	90,		e 90,	•	е 90,	•	e 90,	•	Sequence 90, Appl	Sequence 93, Appl

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Sequence 149, Application US/08857946
Patent No. 5994075
GENERAL INFORMATION:
                                                                                                                                                     NAME: Kathleen M. Williams
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3529/05573
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEPAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 149:
                    MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/017,824
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,946
FILLING DATE: 16-MAX-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NERAL INFORMATION: P.N. APPLICANT: GOODEFILOW, P.N. TITLE OF INVENTION: METHODS TITLE OF INVENTION: GENE OF REQUENCES: 162
                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 38 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                             TOPOLOGY:
                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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Mismatches

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Gaps

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Length 38; Indels

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STREET:

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RESULT 3
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                                                                                                        Sequence 150, Application US/08857946 Patent No. 5994075
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Best Local :
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                                                                          GENERAL INFORMATION:
APPLICANT: Goodfe
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/85'
FILING DATE: 16-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/01:
APPLICATION UMBER: 60/01:
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Ploppy disk
COMPOTIER: ISM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOrdPerfect 6.1
CURRENT APPLICATION DATA:
                CORRESPONDENCE ADDRESS
                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7111
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                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kathleen M. Williams REGISTRATION NUMBER: 34,38
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                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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14-NOV-1997
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US-08-970-740-150/c
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US-08-857-946-150
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
               FILING DATE: 14-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8:
FILING DATE: 16-MAY-1997
PRIOR APPLICATION DATA:
                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,74
                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/017,824
PILLING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: 17-MAY-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,94
FILING DATE: 16-MAY-1997
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STREET: 20
STREET: 30
Boston
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STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: 3529/05573
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 nucleic search, using sw model
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Match
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220
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 GenCore version 5.1.6 (c) 1993 - 2005 Compus
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AAV16078
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Million cell updates/sec
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Abn86446 II-lbeta
Aav82770 Double st
Aaq39253 Platelet
Aaq79696 Primer #2
Aaq79089 Primer to
Aav35012 Human end
Aaa27012 Beta-lact
Add19487 Salmo sal
Abz06815 Human leu
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Adg07907 Sense pri
Aav16077 PCR prime
Aaz43408 Murine c-
Aaa05393 PCR prime
Aav16078 PCR prime
Aaz43409 Murine c-
Aaa05394 PCR prime
Adg76401 Nucleotid
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6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4		6.4	6.4	6.4	6.4		6.4		6.4	6.4	6.4	6.4	6.4		6.4	6.8	
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AAQ62886	AAQ30638	AAQ30641	ACC45050	AAQ49319	AAT79653	AAZ27084	ADT01047	ACI46149	ACF03717	AAZ29237	AAZ26085	AAV07765	AAV07766	ABD27463	ABD27462	ABZ91233	ABZ91232	AAZ98564	AAZ98563	AAZ98565	AAZ98562	ADE49029	AAI66200	ABZ06425	
Aaq62886 GGF prime		Aaq30641 Primer 66	Acc45050 Human PRE	Aaq49319 Degenerin		Aaz27084 Saccharom	Adt01047 Novel mut	Aci46149 Human mic	Acf03717 PCR prime		Aaz26085 Human pol	Aav07765 Oligonucl	Aav07766 Oligonucl	Abd27463 H37989-de	Abd27462 H37989-de	Abz91233 Human oli	Abz91232 Human oli	Aaz98564 Human MAP	Aaz98563 Human MAP	Aaz98565 Human MAP	Aaz98562 Human MAP	Ade49029 Human pat	Aai66200 Peptide n	Abz06425 Human leu	

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RESULT 1
ABZ80324
ID ABZ80324
ID ABZ80324
ID ABZ80324
ID ABZ8
XX ABZ8
AC ABZ8
XX Puri
KW Puri
KW cent
KW cent
KW pCR
OS Syntt
XX WO2C
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XX W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2002; 2002WO-AU000700
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The present invention describes a method (M) for generating a substantially homogeneous population of undifferentiated cells a biological sample (BS), which comprises subjecting BS or its

(UC) from sub-sample

Example 10; Page 47; 90pp; English

Generating substantially homogeneous population of undifferentiated cells from sample, by disrupting tissue sample, discriminating cells in population based on size and performing cell-surface marker-discrimination.

WPI; 2003-140465/13.

PF,

Rietze RL;

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RESULT 2
ADQ07907
ID ADQ0
XX ADQ0
AC ADQ0
XX Sens
XX Anti
KW Panc
XX Unid
XX Unid
XX Unid
XX WO20
XX Unid
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PD 22-J
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The invention relates to a modified human hepatic cell, which is insulin-
producing. Further disclosed is an insulin-producing cell line designated
FH-B-TPN, a method of making an insulin-producing cell line, a method of
treatment of type I diabetes, a method of making insulin in-vitro, and a
vector for the expression of pancreatic duodenal homeobox gene-1 (Pdx1),
                                                                                                                                                                                                                                                                                                                            New modified human hepatic cell, which is insulin-producing, useful as medicament for treating insulin-dependent diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antidiabetic; human hepatic cell; insulin; FH-B-TPN; type 1; diabetes; pancreatic duodenal homeobox gene-1; Pdx 1; insulin-dependent; PCR;
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100.0%; Prr
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Best Local (
                           anterior segment malformations most commonly characterised by eye development defects broadly described as aniridia. The disease is dominant. A population of male mice were treated with ENU to provide a source of mutant PAX6 and a heterozygotic F1 generation produced. Pluorescent single strand conformation polymorphism (SSCP) is utilised to identify those members of the F1 population carrying PAX6 mutations. The method provides mutational screening based on genomic and genetic techniques rather than on phenotypic observation. The method identifies and characterises genes via mutagenesis to identify genes encoding products which may have therapeutic benefit. The method also identifies the presence of mutations in a gene which do not rely solely upon prior matching of a gene with a disease. Heterozygotic organisms can also be screened to identify those carrying a mutation in a copy of a gene of interest even though the gene may be recessive and therefore causes no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid sample from a mutated organism for a mutation in a gene of interest without the prior observation of a phenotypic alteration in the mutated organism resulting from the mutation. PAX6 mutations lead to a variety of the mutation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           where the vector is a lentiviral vector. The modified human hepatic cell is useful for treating insulin-dependent diabetes. Sequences given in records for AD007888-AD007961 represent primers for the RT-PCR analysis of RNA extracted from cultured cells, mature human hepatocytes, and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                observation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 11; Page 58; 66pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification of mutation(s) in genes of interest - without observation of phenotypic alteration in the mutated organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primers AAV16059-76 were used to identify PAX6 mutations in mice ng the method of the invention. The method comprises testing a nud sample from a mutated organism for a mutation in a gene of integer
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/mol_type="unassigned DNA"
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Takagi, M., Shinji, H. and Ota, K.
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Patent: JP 2001292776-A 2 23-OCT-2001,
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